

Supplementary Table 1 Sources of endophytic and rhizospheric bacteria obtained from different banana cultivars maintained at ICAR-NRC for Banana Tiruchirappalli

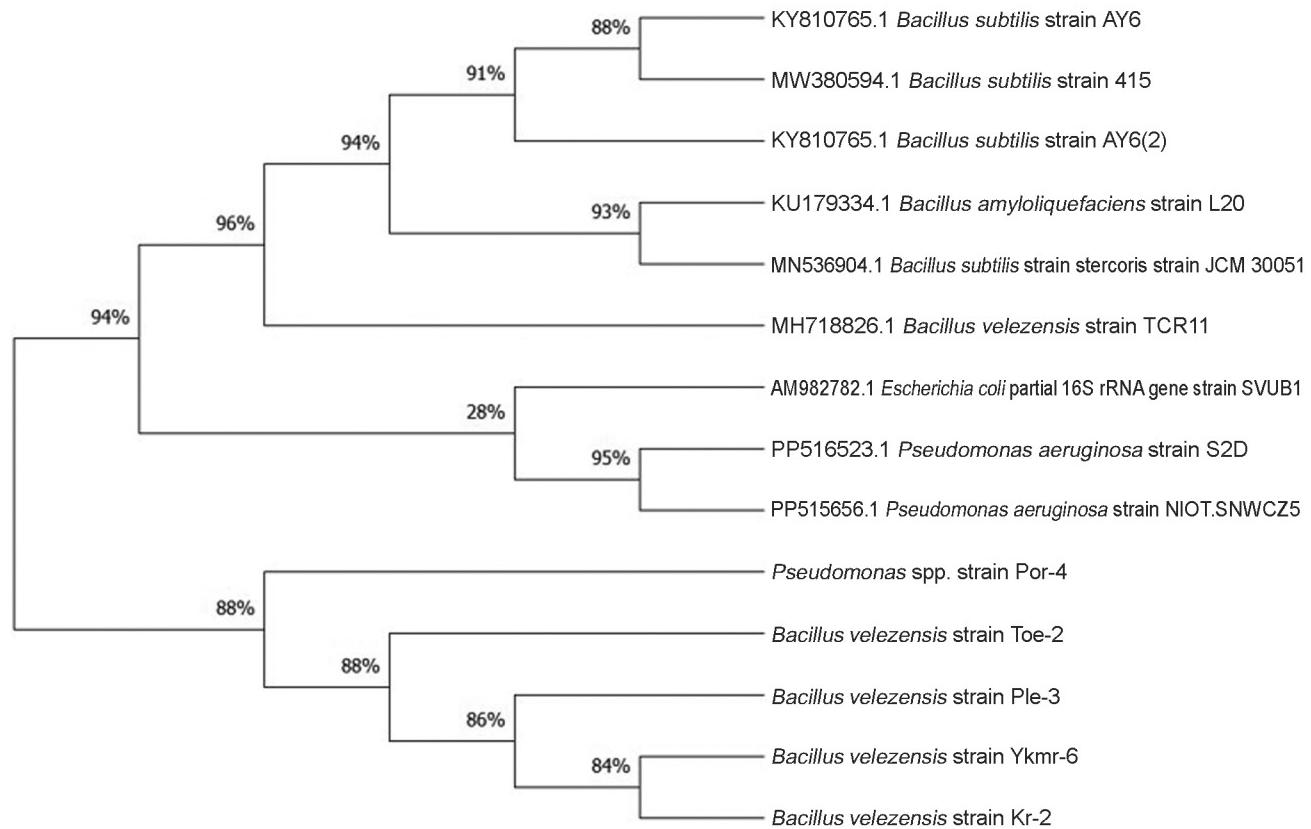
Name of the banana germplasms	Genomic status	Number of isolates		
		Endophytic		Rhizo-spheric
		Root	Corm	
Matti	AA	2	1	1
Pisang Lilin	AA	1	0	2
Pisang Berlin	AA	1	1	2
cv. Rose	AA	2	2	1
Pisang Jari Buaya	AA	2	0	2
Tongat	AA	3	2	3
Yankambi km 5	AAA	4	2	2
Poovan	AAB	3	2	1
Dudh Sagar	AAB	2	0	1
Pisang Ceylon	AAB	3	0	2
Kalibo	AAB	0	3	2
Bhimkol	AAB	2	1	1
Balukpong Wild	AB	2	2	2
Local Peyan	ABB	3	1	2
Burrow Cemsa	ABB	3	0	1
Total	-	33	17	25

Supplementary Table 2 Glass house evaluation of individual endophytic and rhizospheric bacterial isolates against *Foc* TR4

Treatment	Height (cm)	Girth (cm)	Total no. of leaves	Leaf area (cm ²)	Total no. of roots	Internal score (0–5 scale)
<i>Bacillus subtilis</i> (Ple-3)	22.80 ^b (21.28)	7.40 ^{ab} (32.14)	6.40 ^{bc} (28.0)	387.84 ^b (60.32)	14.00 ^{de} (12.90)	3.00 ^c
<i>Bacillus subtilis</i> (Ykmr-6)	21.40 ^c (13.83)	7.40 ^{ab} (32.14)	6.60 ^{bc} (32.0)	475.36 ^a (96.49)	17.80 ^a (43.55)	3.00 ^c
<i>Pseudomonas</i> sp. (Por-4)	25.80 ^a (37.23)	8.00 ^a (42.85)	7.60 ^a (52.0)	381.12 ^b (57.54)	15.40 ^{cd} (24.19)	2.00 ^d
<i>Bacillus subtilis</i> (Kr-2)	21.20 ^c (12.77)	7.40 ^{ab} (32.14)	6.00 ^c (20.0)	384.32 ^b (58.86)	16.20 ^{bc} (30.65)	3.20 ^c
<i>Bacillus velezensis</i> (Toe2)	22.20 ^{bc} (18.09)	7.20 ^{bc} (28.57)	7.00 ^{ab} (40.0)	404.80 ^b (67.33)	17.20 ^{ab} (38.71)	4.00 ^c
<i>Foc</i> TR4 alone	18.80 ^d (0.00)	6.60 ^c (0.00)	5.00 ^d (0.00)	241.92 ^c (0.00)	12.40 ^f (0.00)	5.00 ^a
Uninoculated control	21.00 ^c (11.70)	5.60 ^d (21.28)	6.00 ^c (20.0)	391.68 ^b (61.90)	13.80 ^{ef} (11.29)	0.00 ^e
SEm±	0.41	0.21	0.31	12.48	0.48	0.07
CD (<i>P</i> =0.01)	1.64	0.86	1.21	48.81	1.91	0.29

Values are mean of five replications. Figs in parentheses are per cent increase over *Foc* TR4 alone inoculated control plants. Mean ratings within a column that are followed by the same letter are not significantly different according to LSD at *P*≤0.05.





Supplementary Fig. 1 Phylogenetic tree constructed using neighbour joining tree method with 1000 bootstrap values.